





Hadoop for Scientific Workloads

Lavanya Ramakrishnan

Shane Canon

Shreyas Cholia

Keith Jackson

John Shalf

Lawrence Berkeley National Lab







Example Scientific Applications

- Integrated Microbial Genomes (IMG)
 - analysis of microbial community metagenomes in the integrated context of

all public reference isolate microbial genomes

- Supernova Factory
 - tools to measure expansion of universe and energy
 - task parallel workflow, large data volume
- MODerate-resolution Imaging Spectroradiometer (MODIS)
 - two MODIS satellites near polar orbits
 - > ~ 35 science data products including atmospheric and land products
 - products are in different projection, resolutions (spatial and temporal),
 different times



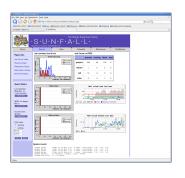
















 Unlimited need for compute cycles and data storage

 Tools and middleware to access resources

HPC and IT resources

Does cloud computing

- >make it easier or better to do what we do?
- ➤help us do things differently than before?
- ➤help us include other users?







Magellan - Exploring Cloud Computing



- Test-bed to explore Cloud Computing for Science
- National Energy Research Scientific Computing Center (NERSC)
- Argonne Leadership Computing Facility (ALCF)

Funded by DOE under the American Recovery and

Reinvestment Act (ARRA)









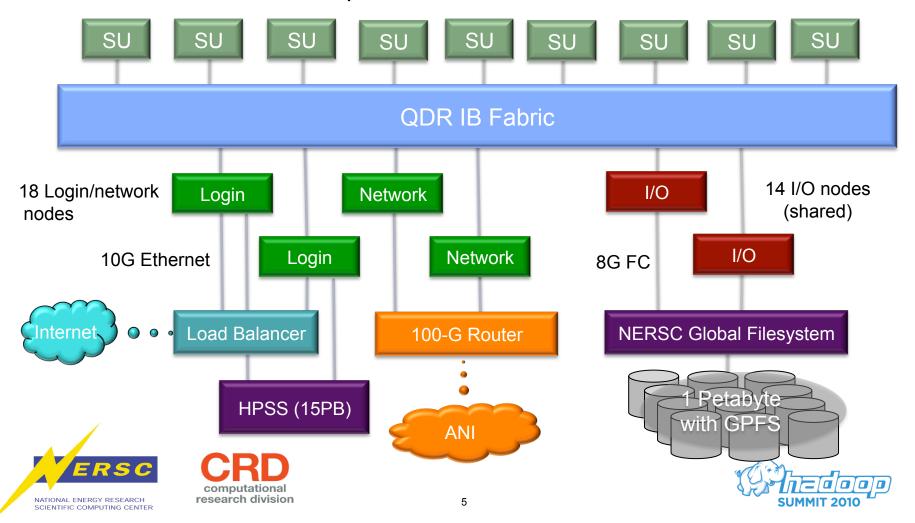






Magellan Cloud at NERSC

720 nodes, 5760 cores in 9 Scalable Units (SUs) → 61.9 Teraflops SU = IBM iDataplex rack with 640 Intel Nehalem cores







- What are the unique needs and features of a science cloud?
- What applications can efficiently run on a cloud?
- Are cloud computing programming models such as Hadoop effective for scientific applications?
- Can scientific applications use a data-as-a-service or software-as-a-service model?
- Is it practical to deploy a single logical cloud across multiple DOE sites?
- What are the security implications of user-controlled cloud images?
- What is the cost and energy efficiency of clouds?













Classes of applications

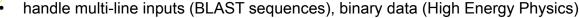
- > tightly coupled MPI application, loosely couple data intensive science
- use batch queue systems in supercomputing centers, local clusters and desktop

Advantages of Hadoop

- transparent data replication, data locality aware scheduling
- fault tolerance capabilities

Mode of operation

- use streaming to launch a script that calls executable
- HDFS for input, need shared file system for binary and database
- input format





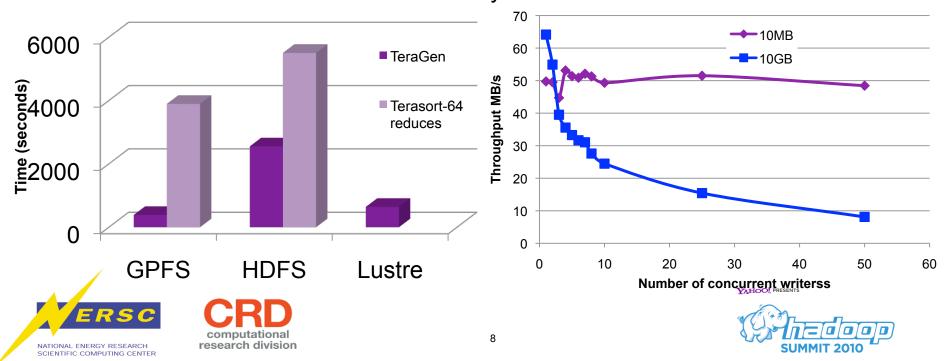






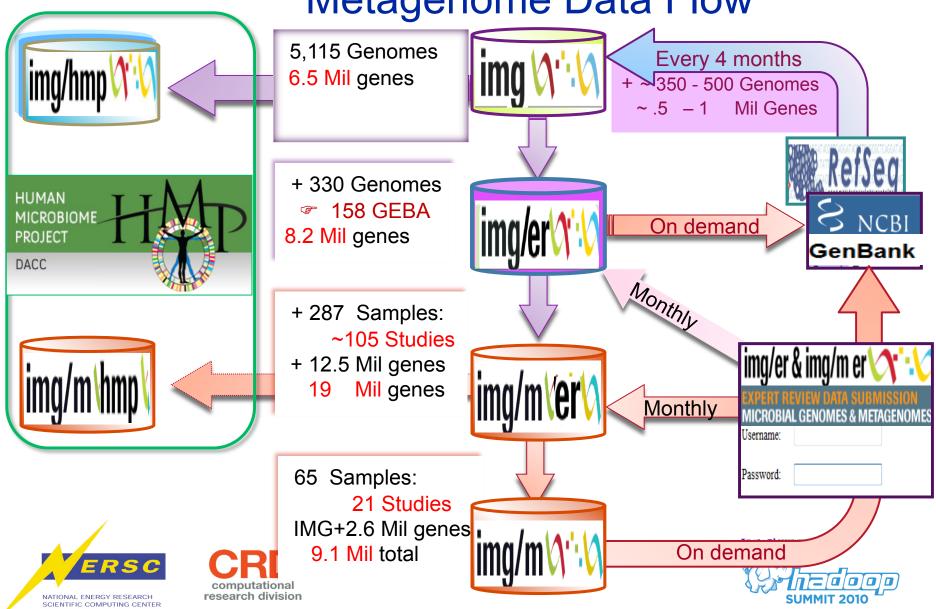
Hadoop Benchmarking: Early Results

- Compare traditional parallel file systems to HDFS
 - 40 node Hadoop cluster where each node contains two Intel Nehalem quad-core processors
 - TeraGen and Terasort to compare file system performance
 - 32 maps for TeraGen and 64 reduces for Terasort over a terabyte of data
 - TestDFSIO to understand concurrency





IMG Systems: Genome & Metagenome Data Flow



BLAST on Hadoop



- NCBI BLAST (2.2.22)
 - > reference IMG genomes- of 6.5 mil genes (~3Gb in size)
 - full input set 12.5 mil metagenome genes against reference

BLAST Hadoop

- uses streaming to manage input data sequences
- binary and databases on a shared file system

BLAST Task Farming Implementation

- server reads inputs and manages the tasks
- client runs blast, copies database to local disk or ramdisk once on startup, pushes back results
- advantages: fault-resilient and allows incremental expansion as resources come available







Hardware Platforms



- Franklin: Traditional HPC System
 - 40k core, 360TFLOP Cray XT4 system at NERSC, Lustre parallel filesystem
- Amazon EC2: Commercial "Infrastructure as a Service"
 Cloud
 - Configure and boot customized virtual machines in Cloud
- Yahoo M45: Shared Research "Platform as a Service"
 Cloud
 - 400 nodes, 8 cores per node, Intel Xeon E5320, 6GB per compute node, 910.95TB
 - Hadoop/MapReduce service: HDFS and shared file system
- Windows Azure BLAST "Software as a Service"

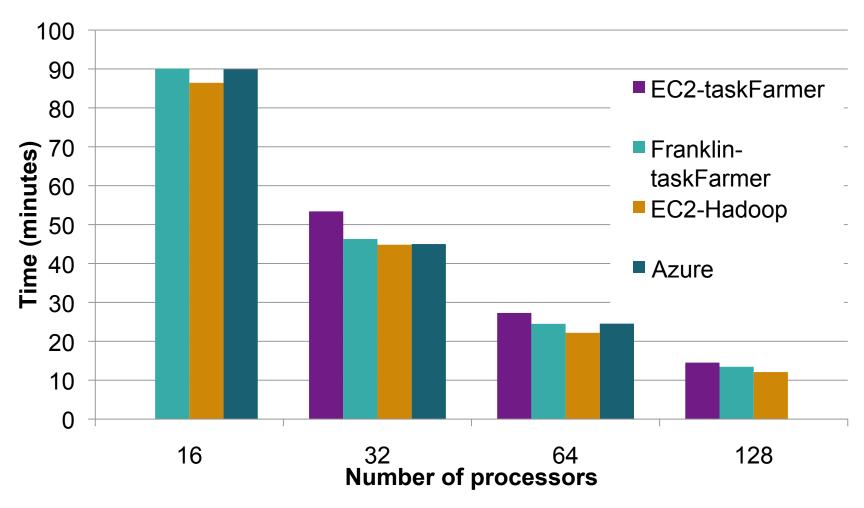




















BLAST on Yahoo! M45 Hadoop

- Initial config Hadoop memory ulimit issues,
 - Hadoop memory limits increased to accommodate high memory tasks
 - 1 map per node for high memory tasks to reduce contention
 - thrashing when DB does not fit in memory
- NFS shared file system for common DB
 - move DB to local nodes (copy to local /tmp).
 - → initial copy takes 2 hours, but now BLAST job completes in < 10 minutes</p>
 - performance is equivalent to other cloud environments.
 - future: Experiment with Distributed Cache
- Time to solution varies no guarantee of simultaneous availability of resources

Strong user group and sysadmin support was key in working through this.











- Output of "all vs. all" pairwise gene sequence comparisons
 - currently data stored in compressed files
 - modifying individual entries is challenging
 - · queries are hard
 - duplication of data to ease presentation by different UI components
- Evaluating changing to Hbase
 - easily update individual rows and simple queries
 - query and update performance exceeds requirements
- Challenge: Bulk loads of approximately 30 billion rows
 - trying multiple techniques for bulk loading
 - best practices are not well documented



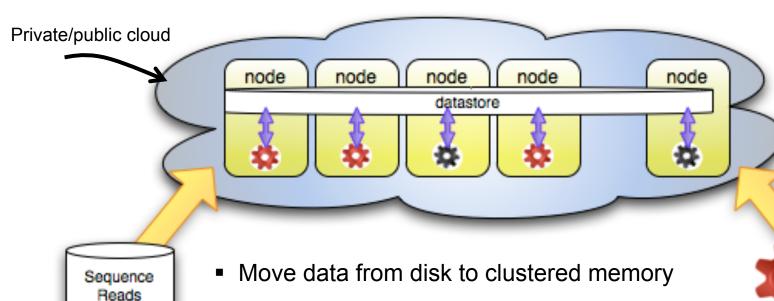




Magellan Application: De-novo assembly

Memory requirements: ~500 GB (de Bruijn graph)

CPU hours (single assembly): velveth: ~23h,velvetg: ~21h



 Move analysis pipeline from single-node to parallel map/reduce jobs



computational research division

efficient horizontal scalability

(more data -> add more nodes)



Source: Karan Bhatia



Metagenomics



Summary



Deployment Challenges

- all jobs run as user "hadoop" affecting file permissions
- less control on how many nodes are used affects allocation policies
- file system performance for large file sizes
- Programming Challenges: No turn-key solution
 - using existing code bases, managing input formats and data

Performance

- BLAST over Hadoop: performance is comparable to existing systems
- existing parallel file systems can be used through Hadoop On Demand
- Additional benchmarking, tuning needed
- Plug-ins for Science











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Questions?

LRamakrishnan@lbl.gov









- On-demand access to computing and cost associativity
- Customized and controlled environments
 - e.g., Supernova Factory codes have sensitivity to OS/compiler versions
- Overflow capacity to supplement existing systems
 - e.g., Berkeley Water Center has analysis that far exceeds capacity of desktops
- Parallel programming models for data intensive science
 - » e.g., BLAST parametric runs









NERSC Magellan Software Strategy



- Runtime provisioning of software images via Moab and xCat
- Explore a variety of usage models
- Choice of local or remote cloud





